Modeling of different scenarios for the spreadof COVID-19 by using the cellular automata

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***Abstract*— In this research, we used the method of mobile cellular automata to study the dynamics of COVID-19. A number of simulation scenarios that take into account different quarantine restrictions are considered and compared. The simulation results revealed that self-isolation regimen is the most effective way to reduce the rate of infection. The simulation model that was developed in the work allows you to easily adapt and take into account new factors of quarantine restrictions.**

Keywords—COVID 19, computational model, simulation, cellular automata, social isolation.

I. INTRODUCTION

Since the end of 2019, with the outbreak of the new COVID-19 virus, the world has completely changed in many aspects: the pandemic has affected the economy, education and science, the healthcare system and global society. Epidemic modeling is usually performed using compartmental models, often referred to as SIR models (Susceptibles–Infected–Recovered), research that began in the works of R. Ross and H. P. Hudson more than a century ago [1], [2] and the work of A. G. McKendrick and W. O. Kermack [3], [4].

Modern modeling strategies provide methods for the prevention and control of infectious diseases and mainly include: (a) isolation measures; (b) routine and practical measures to prevent the epidemic (such as the use of protective masks, ventilation, daily disinfection, etc.); (c) study and job suspension and other preventive and anti-epidemic prevention and control measures.

The paper investigates the simulation of coronavirus infection using mobile cellular automata, which are computational algorithms described by relatively simple local rules. The spread of the epidemic was simulated for different strategies, regimes, and approaches to the spread of the disease, which allows analysis and comparison of the restrictions imposed to control coronavirus infection.

II. REVIEW OF SCIENTIFIC WORKS

Traditionally, most existing mathematical models for modeling epidemics are based on the use of the apparatus of ordinary differential equations, so these models are used for a long time and for a certain period of time to simulate the dynamics of epidemics [4, 5]. Such models distinguish between suspected (S), infected (I) and recovered (R) agents in a particular population and calculate the rate of change in each fraction by solving the system of differential equations [6, 7]. These models have serious drawbacks in the fact that they neglect the local characteristics of the distribution process and do not include the variable susceptibility of individuals. In particular, they cannot properly model individual contact processes, the consequences of individual behavior, the spatial aspects of the spread of the epidemic, and the consequences of mixing patterns of individuals.

One of the main problems of the epidemic process in population dynamics systems is the stochastic nature of its behavior [8]. In addition, there are added modifications of states: mask mode, gatherings in public places, observance of social distance [9-10]. But the mask regime, vaccination and self-isolation are not considered in the complex.

The cellular automata method allows to overcome the shortcomings of the approach using differential equations for modeling infectious diseases, especially with regard to precautions and treatment. Of particular interest are cellular automata that simulate the movement of individuals.

The paper [11] examined the modeling of various infectious conditions of the COVID-19 pandemic using cellular automata, in particular, it was considered the vaccination regime and the possibility of a complete lockdown. Investigations of such scenarios show that strict social isolation is crucial to controlling the pandemic.

In the works [12], the cellular automata method is used to simulate the influenza epidemic COVID-19. Restrictions are imposed in the form of vaccination of susceptible groups of the population and quarantine restrictions; individual mobility is taken into account, but the full range of protection scenarios is not considered.

Therefore, it can be argued that in this situation the most adequate models are obtained when using cellular automata. An important aspect of the cellular automata method is the use of localization. Due to the use of this approach, it will be possible to model with more different restrictions.

III. MATHEMATICAL APPARATUS

Models in which society is divided into groups or classes are called chamber models and are widely used in epidemiology. According to the classic SIR model, there is a set of agents that move and thereby imitate the settlement. The population in this model is divided into three groups depending on the status: S (susceptible) – healthy and susceptible to the disease, I (infected) – infected, which can infect others, R (recovered) – recovered or not susceptible. In this problem, agent go from phase to phase gradually S → I → R.

To model dynamic systems with an epidemic nature, it is necessary to initialize the input data of the modeling environment and initialize agents. We will consider the following parameters:

Environmental of modeling:

- box with a given size (S)
- number of agents (N)
- modeling duration (t)
- infection threshold (p)
- number of infected agents initially *(n_inf)*
- initial position of infected and uninfected agents $\left(L = l_{i=1,N_{sim}}(x,\ y)\right)$

A tuple of the agent:

- agent position $(x,\ y)$
- size of the agent (s)
- speed of movement $(\overline{v})$
- the direction of movement (k)
- the radius of infection (r)
- the agent is infected (inf)
- the agent is vaccinated (vac)
- agent wears a mask $(mask)$
- the agent on self-isolation in case of illness $(isol)$

One of the most important aspects of modeling is comparing computer time and linear dimensions with relevant real data. In particular, if the population of the city is P_s and its area is – S_s then on average persons N_{sim} of this settlement live on the area [13]: $S_{sim} = \frac{N_{sim}}{P_s} S_s$.

If in the simulation model this area is represented as a square with a side $L = 1$, then it will correspond to the true size: $L_{sim} = \sqrt{S_{sim}}$.

Then the distance required for infection will be defined as $\Delta = d_{real} \frac{L}{L_{sim}}$, where d_{real} – real distance in meters, necessary for infecting people. This value is known in medical directories and depends on the type of virus that is simulated.

Assuming that is the average speed of a person $\overline{v}_{real} = 4\ \frac{km}{h}$, then in the simulation model it will correspond to the speed: $\overline{v} = \overline{v}_{real} \frac{L}{L_{sim}}$.

The next step is to determine the duration of one iteration. It should be of such kind: during one iteration a person cannot overcome a distance greater than d, since in this case the agents moving towards each other will slip through each other without interaction. Not enough time – significantly slows down the calculation $\Delta t < \frac{d}{\overline{v}}$. This value allows us to vTcompare the true duration of the disease: $T_{il} = \frac{T_{real}}{\Delta t}$, where T_{real} – the real average duration of the disease.

Using a random number generator with a normal distribution, the positions of agents (and their initial speeds are generated: $L = l_{i=1,N_{sim}}(x,\ y,\ \overline{v},\ k,\ S_{sir},\ r)$, where $x,\ y$ – agent coordinates, $\overline{v}$ - speed of movement, k – the direction of movement, S_{sir} – agent status, r – the number of people infected with this agent ($r = 0$ at the initialization stage).

All agents in the first step of iteration, as a rule, have the S status. One random agent receives status I. Depending on the type of disease, some agents may have R status on the first iteration, which is interpreted as immune sensitive. The next step is to imitate the movement of people. To do this on each iteration, the agent moves to $s = (x + \overline{v}\Delta t,\ y + \overline{v}\Delta t)$. After calculating the position of the agents at the next step of the iteration, the following situations are possible:

1. The agent is nearby or has crossed the simulation boundary. In this case, you can either simulate a mirror reflection (change the sign of one of the components of the velocity to the opposite direction), or aim the agent in the opposite direction (change the signs of both speed components to opposite).
2. The uninfected agent fell into the danger zone of the infected agent. In this case, the following two situations are possible:

- no actions are taken against the agent if it has the R status;
- if the agent has the S status, the value z is determined by the random number generator and taken from the interval $z = [0,1]$. If $z < p$, the person is marked as infected and receives status I, and the value of r of the infected agent increases by 1. The future time of disease of a particular agent is calculated: $T_{il}^{i} = T_{il} + 2t_{il}(z_i - 0.5)$, where z_i – is a random number within $[0,1]$, t_{il} – the possible range of disease duration.

3. People collided or approached a dangerous distance from each other. In this case, it seems most logical to ignore such a situation and allow the passage of a person through a person. At the same time, you can simulate an "elastic collision", when the velocity vectors change the signs to the opposite.
4. The simulation continues until all infected agents recover or die. If the status of an agent is I and the time of the disease is $t_{il}^{i} \geq T_{il}^{i}$, then is determined a random number: $P_d = [0,1]$. If $P_d > D$, the agent recovers, that is, changes the state to R, otherwise it dies and is removed from the calculations.

IV. SIR MODEL MODIFICATIONS

Modification of the model on the basis of mobile cellular machines provides for:

a) Changing the rules of interaction of agents (infection, mask mode, etc.);

b) Modification of agents' behavior (isolation, quarantine, public places with close contact, conscious observance of a safe distance, etc.);

c) Change in the condition of pathogens depending on the time (course of the disease, incubation period, etc.).

1. *Isolation modeling*

Isolation involves creating conditions under which an ill agent cannot infect others. This can be implemented either through additional status and verification at each step of the iteration, or by creating another simulation zone in which all ill agents will be transferred, and allow them to move and interact according to classical rules.

It is necessary to enter an additional parameter T_{inc}(incubation period) to take into account these factors. The value of this parameter T_{real}^{inc} is determined by taking real and well-known time for various diseases $T_{real} = \frac{T_{real}^{inc}}{\Delta t}$.

To take into account the asymptomatic course of the disease during initialization, it is enough for each agent to assign an additional binary status I_s, which will determine how this agent will experience the disease in case of infection

($True$ — asymptomatic, $False$ — with symptoms). This status will be determined depending on the likelihood of asymptomatic disease p_{sym}, which is a known medical quantity for various diseases:

$$I_s = \vdash_{True,\, z<p_{sym}}^{False,\, z\geq p_{sym}}$$

If $I_s = True$, the agent will not be selected in case of infection. Another important value is the number of infected agents I_{max} at which isolation begins. If the total number of infected agents is less than I_{max}, the isolation process does not begin.

1. *Mask regime modeling*

To take into account the mask mode parameter during modeling, we will reduce the risk of infection of the agent using a constant $Q_{mask} = 0.6$. This constant will be multiplied by p and the probability of infection will be calculated as $z < pQ_{mask}$, where $z = [0,1]$ is a random variable.

2. Vaccination modeling

To take into account the vaccination parameter during modeling, we will reduce the risk of infection of the agent using a constant $Q_{vacination} = 0.4$. This constant will be multiplied by p and the probability of infection will be calculated as $z < pQ_{vaccination}$, where $z = [0,1]$ is a random variable.

V. Model formalization

The process of modeling in this model will be modeled until there is no infected agent left. When analyzing different scenarios, it is necessary to run an imitation model not from the first iteration, but from a specific fixed point of time. Therefore, the generation of multi-agent systems in an object-oriented programming language allows at any time during modeling to store all objects on the hard disk and use them as initial values in further analysis of various situations by the methods of model ensembles.

The output of the model is the dynamics of such indicators as the total number of infected, those who recovered and dead agents. Such statistics are kept in general throughout the model.

An important indicator of the dynamics of the epidemic is the basic R_0 and effective reproductive number R. The baseline number of reproductions R_0 is used to measure the potential for transmission of the disease. This is the average number of secondary infections caused by a typical case of infection in a population where everyone is susceptible. In order for an epidemic to occur in a susceptible population, there must be $R_0 > 1$, so the number of cases increases. This is measured by an effective reproduction factor R — the average number of secondary cases for an infectious case in a population consisting of both sensitive and insensitive hosts. If $R > 1$, the number of cases will increase, for example, at the beginning of the epidemic. Where $R = 1$, the disease is endemic, and with $R < 1$, there will be a decrease in the number of cases.

The effective number of reproductions can be estimated by the product of the main reproductive number and the proportion of the susceptible population of the host x.

VI. Results of the modeling

To analyze the spread of COVID-19 and to study in detail all aspects, various modeling options were carried out and the relevant factors were taken into consideration.

Environmental of modeling:

S =810, N=100, t=number of infected agents > 0, p=0.5, n_inf=5, L=list of agents.

A tuple of the agent:

coordinates of the agent - (x, y), $s = 15$, $\overline{v} = 1$, $r = 60$, $k = random(0{,}360))$, $inf = True/False$, $vac = True/False$, $mask = True/False$, $isol = True/False$.

1. Scenarios of the modeling

Simulation 1. Only the mask mode is taken into account.

Simulation 2. Only the vaccination regimen is taken into account.

Simulation 3. A combination of limiting factors is considered - the mask mode and the vaccination regimen.

Simulation 4. A combination of limiting factors is considered - the mask mode and the self-isolation in case of illness.

Simulation 5. Self-isolation in case of illness the vaccination regimen is considered.

Simulation 6 (main). People move freely around the city. Limiting factors such as mask regime, self-isolation and vaccination regimen are taken into account. The possibility of self-isolation for infected people is considered.

2. Analyses of the result

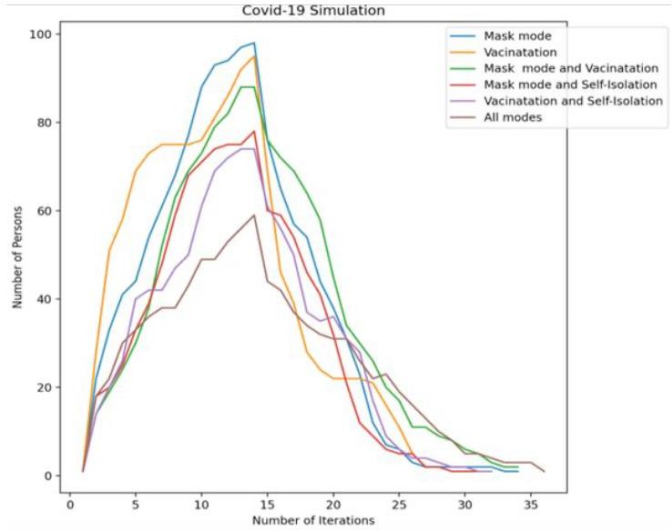

Fig. 1. Dynamics of the number of infected agents in different scenarios

The results of modeling the dynamics of the number of infected agents in different scenarios are presented in Fig. 1.

Scenario (simulation 1), where only the mask mode is considered has the highest incidence peak among all presented simulation scenarios. In this scenario, the number of infected agents increases sharply, critically burdening the medical system. This means that there is an epidemic of overcrowding. In this case, the results are unfavorable, the introduction of only the mask regime is insufficient.

Taking into account only the vaccination regimen (Simulation 2), the number of infected agents also has one of the largest peaks. We observe that the number of infected agents is growing sharply and there is a potential burden on the medical system. Then there is a decrease in the number of infected agents due to the recovery of some agents and their acquisition of immunity as a result of vaccination. Vaccination without other restrictions is ineffective.

In the following case (Simulation 3) the scenario in which the combination of a mask mode and vaccination is considered. The peak number of infected agents is also one of the largest.

Consider the scenario of self-isolation in case of illness and the mask mode (Simulation 4). In this case, we obtain that there is no large peak in the number of infected agents, and the disease progresses more smoothly. This combination of restrictions has reduced the burden on the medical system and avoided overcrowding.

In the case (Simulation 5), self-isolation regimens and vaccination are considered. From the graph, we can conclude that there is no rapid peak in the number of infected agents, as in the first three scenarios simulations and the development of the disease is smoother at the beginning of its spread. This combination of restrictions has reduced the burden on the medical system and is more favorable for the region.

The best situation is in the main scenario (Simulation 6). Development of the disease is smoother. The peak of the epidemic is slightly shifted in time compared to the worst-case scenarios. In the basic simulation scenario, the number of iterations required to complete the application simulation is greater than in other simulation modes. This means that the epidemic process stretches over time. The results of this modeling allow us to conclude that the introduction of vaccination, self-isolation and mask regime in the complex is one of the key means of controlling the pandemic.

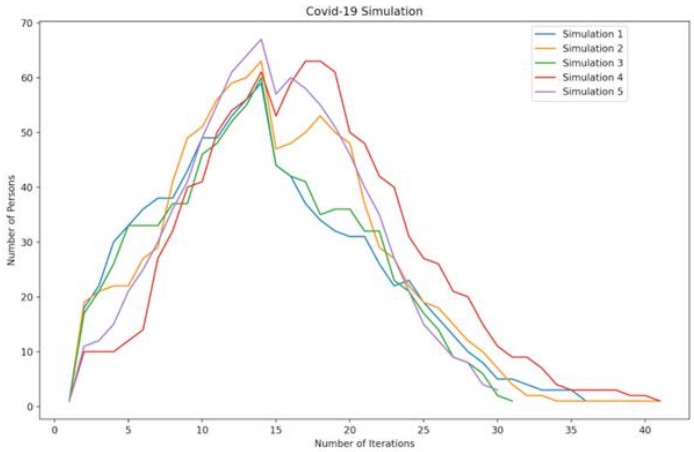

Fig. 2. Dynamics of the number of infected agents of the main model in different simulations

In fig. 2 shows 5 different simulations of the dynamics of the number of infected agents in the main model to demonstrate its stability. The x-axis shows the number of iterations of the simulation, and the y-axis shows the number of infected agents. It is observed that due to a combination of limiting factors in the main model it was possible to reduce the peak number of infected agents from 80-100 people in the first scenario to 67 people in the worst case.

Consider analysis of the stability of the simulation of the number of infected agents of the main model depending on the number of iterations. The maximum peak value of infected agents is 67 for 16 iterations, and the minimum peak value is 59 for 13 iterations in 5 simulation series. The error of the number of infected in the new simulation is +/- 4 agents relative to the average peak value of 62.4. Note also that the average peak value of infected 62.4 agrees well with the maximum peak of infected agents 60 by 13 iterations in the comparative scheme in Fig. 2.

VII. CONCLUSIONS

In this paper the multi-agent model of the dynamics of the spread of epidemic processes was improved. The model is based on the concept of the epidemic process: the presence of a source of infection, transmission mechanism and susceptible organism to the disease. We use a generalized mathematical SIR model and modeling of cellular automata to study the dynamics of infectious diseases and apply it in the context of the spread of COVID-19.

The obtained results are analyzed about the optimal combination of quarantine restrictions to reduce the risk of reaching a rapid peak in the region. The simulation results revealed that disease self-isolation regimens are effective measures to combat the spread of infectious diseases. The application of a set of measures and quarantine restrictions avoids a rapid increase in the course of the disease and strongly affects the position and peak size of infected agents.

The stability of the model depending on different simulations is proved, which allows us to use it in further

researches. The simulation model developed in the work allows the implementation of various strategies to combat the spread of the disease and has the ability to adapt easily expand with new factors.

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